

SEQUENCE LISTING

<110> Russell, William
Klaenhammer, Todd

<120> LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE SAME

<130> 5051.514

<150> 60/206,372
<151> 2000-05-23

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 2150

<212> DNA

<213> Lactobacillus gasseri

<220>

<221> CDS

<222> (153)..(1946)

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agagaaaaca ttacttagaaa ggaaaatcat ct atg gaa tct gca cta tat cca 173
Met Glu Ser Ala Leu Tyr Pro
1 5

att caa aat aaa tat cgg ttt aac act tta atg aat ggc act tgg caa 221
Ile Gln Asn Lys Tyr Arg Phe Asn Thr Leu Met Asn Gly Thr Trp Gln
10 15 20

ttt gaa act gat cct aac tct gtt ggt ctt gac gag gga tgg aat aaa 269
Phe Glu Thr Asp Pro Asn Ser Val Gly Leu Asp Glu Gly Trp Asn Lys
25 30 35

gag ttg cct gat cct gaa gaa atg cct gta cca ggt acg ttt gca gaa 317
Glu Leu Pro Asp Pro Glu Glu Met Pro Val Pro Gly Thr Phe Ala Glu
40 45 50 55

tta act act aag cga gac cgt aaa tac tat act gga gac ttt tgg tat 365
Leu Thr Thr Lys Arg Asp Arg Lys Tyr Tyr Thr Gly Asp Phe Trp Tyr
60 65 70

caa aaa gac ttc ttt att cct tca ttt cta aag aag aaa gaa ctt tat 413
Gln Lys Asp Phe Phe Ile Pro Ser Phe Leu Lys Lys Glu Leu Tyr
75 80 85

atc cgt ttt ggt tcg gtt act cat cgc gca aaa gta ttt att aat gga 461
Ile Arg Phe Gly Ser Val Thr His Arg Ala Lys Val Phe Ile Asn Gly
90 95 100

cat gaa gtc ggt caa cat gaa ggt ggt ttt tta cca ttt caa gta aaa 509
His Glu Val Gly Gln His Glu Gly Phe Leu Pro Phe Gln Val Lys

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105	110	115	
att tca aat tat att aat tac gac caa act aat cgt gta act gtt tta Ile Ser Asn Tyr Ile Asn Tyr Asp Gln Thr Asn Arg Val Thr Val Leu 120 125 130 135			557
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gca aca att acc tac aat atc gag gca aat aat aat gct gaa ttt aaa Ala Thr Ile Thr Tyr Asn Ile Glu Ala Asn Asn Asn Ala Glu Phe Lys 200 205 210 215			797
gta aca ctt ttc gat aat caa aaa gaa gta gcg tgt gct act tct aaa Val Thr Leu Phe Asp Asn Gln Lys Glu Val Ala Cys Ala Thr Ser Lys 220 225 230			845
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gat ccg tat tca tac aaa ata aag att gaa atg ctc gaa gac gga aaa Asp Pro Tyr Ser Tyr Lys Ile Lys Ile Glu Met Leu Glu Asp Gly Lys 250 255 260			941
aca gtt gac gaa tac aca gat aaa att ggt atc cgc aca gtt aaa att Thr Val Asp Glu Tyr Thr Asp Lys Ile Gly Ile Arg Thr Val Lys Ile 265 270 275			989
gtg aat gat aaa atc ttg ctc aat aat cac cca att tat tta aaa ggc Val Asn Asp Lys Ile Leu Asn Asn His Pro Ile Tyr Leu Lys Gly 280 285 290 295			1037
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gcc gat aaa tat ggc ttt tta att att gat gaa gta ccc gct gtt ggt Ala Asp Lys Tyr Gly Phe Leu Ile Ile Asp Glu Val Pro Ala Val Gly 345 350 355			1229
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tcg cac ttt ttt gct tcg aaa act gtg cct gaa tta aaa aag gtc cat Ser His Phe Phe Ala Ser Lys Thr Val Pro Glu Leu Lys Lys Val His 380 385 390	1325
gaa caa gaa ata aaa gaa atg atc gat cgc gac cag cgt cac cct tca Glu Gln Glu Ile Lys Glu Met Ile Asp Arg Asp Gln Arg His Pro Ser 395 400 405	1373
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taatatttta gttttcacaa ataatcgatgc tcaattaaaa ataatcgata tcatttttagt	2006
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<212> PRT
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35 40 45

Val Pro Gly Thr Phe Ala Glu Leu Thr Thr Lys Arg Asp Arg Lys Tyr
50 55 60

Tyr Thr Gly Asp Phe Trp Tyr Gln Lys Asp Phe Phe Ile Pro Ser Phe
65 70 75 80

Leu Lys Lys Lys Glu Leu Tyr Ile Arg Phe Gly Ser Val Thr His Arg
85 90 95

Ala Lys Val Phe Ile Asn Gly His Glu Val Gly Gln His Glu Gly Gly
100 105 110

Phe Leu Pro Phe Gln Val Lys Ile Ser Asn Tyr Ile Asn Tyr Asp Gln
115 120 125

Thr Asn Arg Val Thr Val Leu Val Asn Asn Glu Leu Ser Glu Lys Ala
130 135 140

Ile Pro Cys Gly Thr Glu Glu Ile Leu Asp Asn Gly Gln Lys Leu Ala
145 150 155 160

Gln Pro Tyr Phe Asp Phe Asn Tyr Ser Gly Ile Met Arg Asn Val
165 170 175

Trp Leu Leu Ala Leu Pro Gln Ser Gln Ile Thr Asn Phe Lys Leu Asn
180 185 190

Tyr Gln Leu Ala Asn Asn Lys Ala Thr Ile Thr Tyr Asn Ile Glu Ala
195 200 205

Asn Asn Asn Ala Glu Phe Lys Val Thr Leu Phe Asp Asn Gln Lys Glu
210 215 220

Val Ala Cys Ala Thr Ser Lys Asn Thr Ser Ser Leu Thr Ile Lys Asn
225 230 235 240

Pro His Leu Trp Ser Pro Asn Asp Pro Tyr Ser Tyr Lys Ile Lys Ile
245 250 255

Glu Met Leu Glu Asp Gly Lys Thr Val Asp Glu Tyr Thr Asp Lys Ile
260 265 270

Gly Ile Arg Thr Val Lys Ile Val Asn Asp Lys Ile Leu Leu Asn Asn
275 280 285

His Pro Ile Tyr Leu Lys Gly Phe Gly Lys His Glu Asp Phe Asn Val
290 295 300

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Leu Gly Lys Ala Val Asn Glu Ser Ile Ile Lys Arg Asp Tyr Glu Cys
305 310 315 320

Met Lys Trp Ile Gly Ala Asn Cys Phe Arg Ser Ser His Tyr Pro Tyr
325 330 335

Ala Glu Glu Trp Tyr Gln Tyr Ala Asp Lys Tyr Gly Phe Leu Ile Ile
340 345 350

Asp Glu Val Pro Ala Val Gly Leu Asn Arg Ser Ile Thr Asn Phe Leu
355 360 365

Asn Val Thr Asn Ser Asn Gln Ser His Phe Phe Ala Ser Lys Thr Val
370 375 380

Pro Glu Leu Lys Lys Val His Glu Gln Glu Ile Lys Glu Met Ile Asp
385 390 395 400

Arg Asp Gln Arg His Pro Ser Val Ile Ala Trp Ser Leu Phe Asn Glu
405 410 415

Pro Glu Ser Thr Thr Gln Glu Ser Tyr Asp Tyr Phe Lys Asp Ile Phe
420 425 430

Ala Phe Ala Arg Lys Leu Asp Pro Gln Asn Arg Pro Tyr Thr Gly Thr
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Leu Val Met Gly Ser Gly Pro Lys Val Asp Lys Leu His Pro Leu Cys
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Asp Phe Val Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Ala Gly Gly
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Pro Glu Ile Val Asn Ala Lys Lys Met Leu Glu Asp Glu Leu Asp Gly
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Ala Asp Thr Leu Ser Ser Ser His Arg Leu Pro Asp Glu Met Trp Ser
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Gln Glu Tyr Gln Asn Glu Tyr Tyr Gln Met Tyr Phe Asp Ile Phe Lys
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Lys Tyr Pro Phe Ile Cys Gly Glu Leu Val Trp Asn Phe Ala Asp Phe
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Lys Thr Ser Glu Gly Ile Met Arg Val Gly Gly Asn Asp Lys Gly Ile
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<210> 10
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<210> 11
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<400> 12
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